SEQUENCE LISTING

<110> Gray, Joe
Neve, Richard M.
The Regents of the University of California

<120> Breast Cancer Genes

<130> 023070-139300US

<140> US 10/616,403
<141> 2003-07-08

<160> 7

<170> PatentIn Ver. 2.1

<210> 1
<211> 2182
<212> DNA
<213> Homo sapiens

<220>
<223> Bcl2-associated athanogene 4 (BAG4), Silencer of Death Domains (SODD)

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<210> 2
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<212> PRT
<213> Homo sapiens

<220>
<223> Bcl2-associated athanogene 4 (BAG4), Silencer of
Death Domains (SODD)

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Tyr Gly Arg Tyr Tyr Gly Pro Gly Gly Gly Asp Val Pro Val His Pro
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Pro Pro Pro Leu Tyr Pro Leu Arg Pro Glu Pro Pro Gln Pro Pro Ile
35 40 45

Ser Trp Arg Val Arg Gly Gly Gly Pro Ala Glu Thr Thr Trp Leu Gly
50 55 60

Glu Gly Gly Gly Gly Asp Gly Tyr Tyr Pro Ser Gly Gly Ala Trp Pro
65 70 75 80

Glu Pro Gly Arg Ala Gly Gly Ser His Gln Glu Gln Pro Pro Tyr Pro
85 90 95

Ser Tyr Asn Ser Asn Tyr Trp Asn Ser Thr Ala Arg Ser Arg Ala Pro
100 105 110

Tyr Pro Ser Thr Tyr Pro Val Arg Pro Glu Leu Gln Gly Gln Ser Leu
115 120 125

Asn Ser Tyr Thr Asn Gly Ala Tyr Gly Pro Thr Tyr Pro Pro Gly Pro
130 135 140

Gly Ala Asn Thr Ala Ser Tyr Ser Gly Ala Tyr Tyr Ala Pro Gly Tyr
145 150 155 160

Thr Gln Thr Ser Tyr Ser Thr Glu Val Pro Ser Thr Tyr Arg Ser Ser
165 170 175

Gly Asn Ser Pro Thr Pro Val Ser Arg Trp Ile Tyr Pro Gln Gln Asp
180 185 190

Cys Gln Thr Glu Ala Pro Pro Leu Arg Gly Gln Val Pro Gly Tyr Pro
195 200 205

Pro Ser Gln Asn Pro Gly Met Thr Leu Pro His Tyr Pro Tyr Gly Asp
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Gly Asn Arg Ser Val Pro Gln Ser Gly Pro Thr Val Arg Pro Gln Glu
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Asp Ala Trp Ala Ser Pro Gly Ala Tyr Gly Met Gly Gly Arg Tyr Pro
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Trp Pro Ser Ser Ala Pro Ser Ala Pro Pro Gly Asn Leu Tyr Met Thr
            260                 265                 270

Glu Ser Thr Ser Pro Trp Pro Ser Ser Gly Ser Pro Gln Ser Pro Pro
        275                 280                 285

Ser Pro Pro Val Gln Gln Pro Lys Asp Ser Ser Tyr Pro Tyr Ser Gln
    290                 295                 300

Ser Asp Gln Ser Met Asn Arg His Asn Phe Pro Cys Ser Val His Gln
305                 310                 315                 320

Tyr Glu Ser Ser Gly Thr Val Asn Asn Asp Asp Ser Asp Leu Leu Asp
                325                 330                 335

Ser Gln Val Gln Tyr Ser Ala Glu Pro Gln Leu Tyr Gly Asn Ala Thr
            340                 345                 350

Ser Asp His Pro Asn Asn Gln Asp Gln Ser Ser Ser Leu Pro Glu Glu
        355                 360                 365

Cys Val Pro Ser Asp Glu Ser Thr Pro Pro Ser Ile Lys Lys Ile Ile
    370                 375                 380

His Val Leu Glu Lys Val Gln Tyr Leu Glu Gln Glu Val Glu Glu Phe
385                 390                 395                 400

Val Gly Lys Lys Thr Asp Lys Ala Tyr Trp Leu Leu Glu Glu Met Leu
                405                 410                 415

Thr Lys Glu Leu Leu Glu Leu Asp Ser Val Glu Thr Gly Gly Gln Asp
            420                 425                 430

Ser Val Arg Gln Ala Arg Lys Glu Ala Val Cys Lys Ile Gln Ala Ile
        435                 440                 445

Leu Glu Lys Leu Glu Lys Lys Gly Leu
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<210> 3
<211> 1814
<212> DNA
<213> Homo sapiens

<220>
<223> ADP-ribosylation factor-1 (ARF1)

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aaagaaatgc gcatcctcat ggtgggcctg gatgctgcag ggaagaccac gatcctctac 180
aagcttaagc tgggtgagat cgtgaccacc attcccacca taggcttcaa cgtggaaacc 240
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gcggccgaga tcacagacaa gctggggctg cactcactac gccacaggaa ctggtacatt 540

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<210> 4
<211> 181
<212> PRT
<213> Homo sapiens

<220>
<223> ADP-ribosylation factor-1 (ARF1)

<400> 4

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             20                  25                  30

Ile Leu Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile Pro Thr
         35                  40                  45

Ile Gly Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Ile Ser Phe Thr
     50                  55                  60

Val Trp Asp Val Gly Gly Gln Asp Lys Ile Arg Pro Leu Trp Arg His
 65                  70                  75                  80

Tyr Phe Gln Asn Thr Gln Gly Leu Ile Phe Val Val Asp Ser Asn Asp
                 85                  90                  95

Arg Glu Arg Val Asn Glu Ala Arg Glu Glu Leu Met Arg Met Leu Ala
            100                 105                 110

Glu Asp Glu Leu Arg Asp Ala Val Leu Leu Val Phe Ala Asn Lys Gln
        115                 120                 125

Asp Leu Pro Asn Ala Met Asn Ala Ala Glu Ile Thr Asp Lys Leu Gly
    130                 135                 140
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Leu His Ser Leu Arg His Arg Asn Trp Tyr Ile Gln Ala Thr Cys Ala
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Thr Ser Gly Asp Gly Leu Tyr Glu Gly Leu Asp Trp Leu Ser Asn Gln
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Leu Arg Asn Gln Lys
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<210> 5
<211> 3921
<212> DNA
<213> Homo sapiens

<220>
<223> Ephrin Receptor A2 (EPHA2), Epithelial Cell Receptor Protein-Tyrosine Kinase (ECK)

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<210> 6
<211> 976
<212> PRT
<213> Homo sapiens

<220>
<223> Ephrin Receptor A2 (EPHA2), Epithelial Cell
Receptor Protein-Tyrosine Kinase (ECK)

<400> 6

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             20                  25                  30

Asp Phe Ala Ala Ala Gly Gly Glu Leu Gly Trp Leu Thr His Pro Tyr
         35                  40                  45

Gly Lys Gly Trp Asp Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile
     50                  55                  60

Tyr Met Tyr Ser Val Cys Asn Val Met Ser Gly Asp Gln Asp Asn Trp
 65                  70                  75                  80

Leu Arg Thr Asn Trp Val Tyr Arg Gly Glu Ala Glu Arg Asn Asn Phe
                 85                  90                  95

Glu Leu Asn Phe Thr Val Arg Asp Cys Asn Ser Phe Pro Gly Gly Ala
            100                 105                 110

Ser Ser Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Ala Glu Ser Asp Leu
        115                 120                 125
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Asp Tyr Gly Thr Asn Phe Gln Lys Arg Leu Phe Thr Lys Ile Asp Thr
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Ile Ala Pro Asp Glu Ile Thr Val Ser Ser Asp Phe Glu Ala Arg His
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Val Lys Leu Asn Val Glu Glu Arg Ser Val Gly Pro Leu Thr Arg Lys
                165                 170                 175

Gly Phe Tyr Leu Ala Phe Gln Asp Ile Gly Ala Cys Val Ala Leu Leu
            180                 185                 190

Ser Val Arg Val Tyr Tyr Lys Lys Cys Pro Glu Leu Leu Gln Gly Leu
        195                 200                 205

Ala His Phe Pro Glu Thr Ile Ala Gly Ser Asp Ala Pro Ser Leu Ala
    210                 215                 220

Thr Val Ala Gly Thr Cys Val Asp His Ala Val Val Pro Pro Gly Gly
225                 230                 235                 240

Glu Glu Pro Arg Met His Cys Ala Val Asp Gly Glu Trp Leu Val Pro
                245                 250                 255

Ile Gly Gln Cys Leu Cys Gln Ala Gly Tyr Glu Lys Val Glu Asp Ala
            260                 265                 270

Cys Gln Ala Cys Ser Pro Gly Phe Phe Lys Phe Glu Ala Ser Glu Ser
        275                 280                 285

Pro Cys Leu Glu Cys Pro Glu His Thr Leu Pro Ser Pro Glu Gly Ala
    290                 295                 300

Thr Ser Cys Glu Cys Glu Glu Gly Phe Phe Arg Ala Pro Gln Asp Pro
305                 310                 315                 320

Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro His Tyr Leu Thr
                325                 330                 335

Ala Val Gly Met Gly Ala Lys Val Glu Leu Arg Trp Thr Pro Pro Gln
            340                 345                 350

Asp Ser Gly Gly Arg Glu Asp Ile Val Tyr Ser Val Thr Cys Glu Gln
        355                 360                 365

Cys Trp Pro Glu Ser Gly Glu Cys Gly Pro Cys Glu Ala Ser Val Arg
    370                 375                 380

Tyr Ser Glu Pro Pro His Gly Leu Thr Arg Thr Ser Val Thr Val Ser
385                 390                 395                 400

Asp Leu Glu Pro His Met Asn Tyr Thr Phe Thr Val Glu Ala Arg Asn
                405                 410                 415

Gly Val Ser Gly Leu Val Thr Ser Arg Ser Phe Arg Thr Ala Ser Val
            420                 425                 430

Ser Ile Asn Gln Thr Glu Pro Pro Lys Val Arg Leu Glu Gly Arg Ser
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465                 470                 475                 480

Ser Tyr Asn Val Arg Arg Thr Glu Gly Phe Ser Val Thr Leu Asp Asp
                485                 490                 495

Leu Ala Pro Asp Thr Thr Tyr Leu Val Gln Val Gln Ala Leu Thr Gln
            500                 505                 510

Glu Gly Gln Gly Ala Gly Ser Lys Val His Glu Phe Gln Thr Leu Ser
        515                 520                 525

Pro Glu Gly Ser Gly Asn Leu Ala Val Ile Gly Gly Val Ala Val Gly
    530                 535                 540

Val Val Leu Leu Leu Val Leu Ala Gly Val Gly Phe Phe Ile His Arg
545                 550                 555                 560

Arg Arg Lys Asn Gln Arg Ala Arg Gln Ser Pro Glu Asp Val Tyr Phe
                565                 570                 575

Ser Lys Ser Glu Gln Leu Lys Pro Leu Lys Thr Tyr Val Asp Pro His
            580                 585                 590

Thr Tyr Glu Asp Pro Asn Gln Ala Val Leu Lys Phe Thr Thr Glu Ile
        595                 600                 605

His Pro Ser Cys Val Thr Arg Gln Lys Val Ile Gly Ala Gly Glu Phe
    610                 615                 620

Gly Glu Val Tyr Lys Gly Met Leu Lys Thr Ser Ser Gly Lys Lys Glu
625                 630                 635                 640

Val Pro Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr Thr Glu Lys Gln
                645                 650                 655

Arg Val Asp Phe Leu Gly Glu Ala Gly Ile Met Gly Gln Phe Ser His
            660                 665                 670

His Asn Ile Ile Arg Leu Glu Gly Val Ile Ser Lys Tyr Lys Pro Met
        675                 680                 685

Met Ile Ile Thr Glu Tyr Met Glu Asn Gly Ala Leu Asp Lys Phe Leu
    690                 695                 700

Arg Glu Lys Asp Gly Glu Phe Ser Val Leu Gln Leu Val Gly Met Leu
705                 710                 715                 720

Arg Gly Ile Ala Ala Gly Met Lys Tyr Leu Ala Asn Met Asn Tyr Val
                725                 730                 735

His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val
            740                 745                 750

Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro
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Glu Ala Thr Tyr Thr Thr Ser Gly Gly Lys Ile Pro Ile Arg Trp Thr
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Ala Pro Glu Ala Ile Ser Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val
785                 790                 795                 800

Trp Ser Phe Gly Ile Val Met Trp Glu Val Met Thr Tyr Gly Glu Arg
                805                 810                 815

Pro Tyr Trp Glu Leu Ser Asn His Glu Val Met Lys Ala Ile Asn Asp
            820                 825                 830

Gly Phe Arg Leu Pro Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln
        835                 840                 845

Leu Met Met Gln Cys Trp Gln Gln Glu Arg Ala Arg Arg Pro Lys Phe
    850                 855                 860

Ala Asp Ile Val Ser Ile Leu Asp Lys Leu Ile Arg Ala Pro Asp Ser
865                 870                 875                 880

Leu Lys Thr Leu Ala Asp Phe Asp Pro Arg Val Ser Ile Arg Leu Pro
                885                 890                 895

Ser Thr Ser Gly Ser Glu Gly Val Pro Phe Arg Thr Val Ser Glu Trp
            900                 905                 910

Leu Glu Ser Ile Lys Met Gln Gln Tyr Thr Glu His Phe Met Ala Ala
        915                 920                 925

Gly Tyr Thr Ala Ile Glu Lys Val Val Gln Met Thr Asn Asp Asp Ile
    930                 935                 940

Lys Arg Ile Gly Val Arg Leu Pro Gly His Gln Lys Arg Ile Ala Tyr
945                 950                 955                 960

Ser Leu Leu Gly Leu Lys Asp Gln Val Asn Thr Val Gly Ile Pro Ile
                965                 970                 975
```

<210> 7
<211> 200
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:poly-Gly
flexible linker

<220>
<221> MOD_RES
<222> (6)..(200)
<223> Gly residues from position 6 to 200 may be present
or absent

<400> 7

```
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
  1               5                  10                  15

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
            20                  25                  30
```

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
35 40 45

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
50 55 60

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
65 70 75 80

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
85 90 95

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
100 105 110

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
115 120 125

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
130 135 140

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
145 150 155 160

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
165 170 175

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
180 185 190

Gly Gly Gly Gly Gly Gly Gly Gly
195 200